

ABSTRACT OF THE INVENTION

A method for identifying an unknown base sequence present in a target single-stranded nucleic acid utilizing a probe array in which single-stranded
5 nucleic acid probes are arranged as isolated spots on a substrate, where each probe has a base sequence complementary to one of plural base sequences expected to be the unknown base sequence, and fluorescence pattern of a sample on the probe array is compared with
10 template patterns to know the base sequence of the sample.

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